

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 25, 2000, 20:27:11 ; Search time 90.74 seconds
(without alignments)
485.965 Million cell updates/sec

Title: US-09-125-005-6

Perfect score: 3384

Sequence: 1 MAQSTATSPDGGTTFEHLWS.....PDCKARKOPIKEETFEAIH 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3384	100.0	636	4	O15350 homo sapien
2	3304.5	97.7	637	6	Q9XSK8 cercopithec
3	2624	77.5	499	4	O15351 homo sapien
4	2414.5	71.4	641	13	Q9W654 barbus barb
5	2379	70.3	497	11	Q9WUJ0
6	1789	52.9	680	11	O88898 mus musculu
7	1786	52.8	641	4	O75195
8	1777	52.5	534	11	O35834 rattus norv
9	1743	51.5	586	11	O89097
10	1727	51.0	596	4	O75080
11	1297.5	38.3	484	4	O76078
12	1284.3	38.0	483	11	O88897
13	1248.5	36.9	393	4	O75922
14	1238.5	36.6	389	11	O88899
15	859.5	25.4	564	5	O27937
16	821	24.3	369	13	Q9W678 barbus barb
17	789.5	23.3	376	13	O93379
18	750.5	22.2	378	12	P89002
19	750.5	22.2	391	11	Q9WUR6
20	736.5	21.8	391	6	O36006 marmota mon

21	731.5	21.6	367	13	Q9W679
22	724.5	21.4	393	4	Q16848
23	723.5	21.4	393	4	Q16811
24	720.5	21.3	393	4	Q15087
25	720.5	21.3	393	4	Q16535
26	720.5	21.3	393	4	Q16809
27	720	21.3	281	6	Q29475
28	719.5	21.3	393	4	Q16808
29	718.5	21.2	393	4	Q15086
30	717.5	21.2	393	4	Q16810
31	716.5	21.2	265	13	Q9W682
32	716.5	21.2	393	4	Q16807
33	715.5	21.1	390	11	O70366
34	713.5	21.1	393	4	Q15088
35	712.5	21.1	265	13	Q9W681
36	712.5	21.1	265	13	Q9W680
37	686	20.3	342	13	O57538
38	686	20.3	342	13	O92143
39	685	20.1	285	6	Q95326
40	680.5	20.1	286	12	P90332
41	671.5	19.8	286	12	P89003
42	639.5	18.9	238	12	P89004
43	576	17.0	205	11	O35873
44	573.5	16.9	196	6	Q29484
45	530.5	15.7	146	6	Q29469

ALIGNMENTS

RESULT 1

O15350
ID O15350 PRELIMINARY; PRT: 636 AA.
AC O15350;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE P53-LIKE TRANSCRIPTION FACTOR (P73 PROTEIN).
GN P73 OR TP73.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97433090.
RA KAGHAD M., BONNET H., YANG A., CREANCIER L., BISCAN J.C., VALENT A.,
RA MINTY A., CHALON P., LELIAS J.M., DUMONT X., FERRARA P., MCKEON F.,
RA CAPUT D.;
RT "Monoclonally expressed gene related to p53 at 1p36, a region
RT frequently deleted in neuroblastoma and other human cancers.";
RL Cell 90:809-819(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA YOSHIKAWA H., HAGIWARA K., HARRIS C.C.;
RT "Mutational analysis of p73 and p53 in Human Cancer Cell Lines.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MAI M., HUANG H., REED C., QIAN C., SMITH J.S., ALDERETE B.,
RA JENKINS R., SMITH D.I., LIU W.;
RT "Genomic organization and mutation analysis of p73 in
RT oligodendrogliomas with chromosome 1 p-arm deletions.";
RL Genomics 0:0-0(1998).
RN [4]
DR EMBL; Y11416; CAA72220.1; -;
DR EMBL; Y11416; CAA72221.1; -;
DR EMBL; AF077628; AAC61887.1; -;
DR EMBL; AF077616; AAC61887.1; JOINED.
DR EMBL; AF077617; AAC61887.1; JOINED.
DR EMBL; AF077618; AAC61887.1; JOINED.
DR EMBL; AF077619; AAC61887.1; JOINED.
DR EMBL; AF077620; AAC61887.1; JOINED.
DR EMBL; AF077621; AAC61887.1; JOINED.
DR EMBL; AF077622; AAC61887.1; JOINED.
DR EMBL; AF077624; AAC61887.1; JOINED.

Q9W679 tetraodon m
Q16848 homo sapien
Q16811 homo sapien
Q15087 homo sapien
Q16535 homo sapien
Q16809 homo sapien
Q29475 canis famil
Q16808 homo sapien
Q15086 homo sapien
Q16810 homo sapien
Q9W682 oncorhynch
Q16807 homo sapien
Q70366 mus musculu
Q15088 homo sapien
Q9W681 oncorhynch
Q9W680 oncorhynch
O57538 xiphophorus
Q92143 xiphophorus
Q95326 canis famil
P90332 mastomys na
P89003 mastomys na
P89004 mastomys na
O35873 cricetus
Q29484 equus cabal
Q29469 canis famil

EMBL; AF077625; AAC61887.1; JOINED.
EMBL; AF077626; AAC61887.1; JOINED.
EMBL; AF077627; AAC61887.1; JOINED.
EMBL; AF079094; AAD39696.1; -
EMBL; AF079082; AAD39696.1; JOINED.
EMBL; AF079083; AAD39696.1; JOINED.
EMBL; AF079084; AAD39696.1; JOINED.
EMBL; AF079085; AAD39696.1; JOINED.
EMBL; AF079086; AAD39696.1; JOINED.
EMBL; AF079087; AAD39696.1; JOINED.
EMBL; AF079088; AAD39696.1; JOINED.
EMBL; AF079089; AAD39696.1; JOINED.
EMBL; AF079090; AAD39696.1; JOINED.
EMBL; AF079091; AAD39696.1; JOINED.
EMBL; AF079092; AAD39696.1; JOINED.
EMBL; AF079093; AAD39696.1; JOINED.
HSP; P04637; IFSR.
PFAM; PF00870; P53.
PRINTS; PR00386; P53SUPPRESSR.
SEQUENCE 636 AA; 69623 MW; C770F457 CRC32;

Query Match 100.0%; Score 3384; DB 4; Length 636;

Best Local Similarity 100.0%; Pred. No. 4.4e-263;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVVGTTDSSMDVFHLEGMTTS 60
1 MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVVGTTDSSMDVFHLEGMTTS 60
61 VMAQFNLLSSTMDQSSRAASAPYTPHAAASVPTSHPSYAPQSSFTDMSAPVIPSNTD 120
61 VMAQFNLLSSTMDQSSRAASAPYTPHAAASVPTSHPSYAPQSSFTDMSAPVIPSNTD 120
121 YPGPHFEVTFQSSSTAKSATWYSPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180
121 YPGPHFEVTFQSSSTAKSATWYSPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180
181 YKKAETHVDVVKRCPNHELGRDNFEGOSAPASHLIRVEGNLSQYVDDPVTGROSVVVY 240
181 YKKAETHVDVVKRCPNHELGRDNFEGOSAPASHLIRVEGNLSQYVDDPVTGROSVVVY 240
241 EPPQVGTFTTILYFNFCNSCVGMNRRPILIIITLMDRDGOVLGRSFEGRICACPR 300
241 EPPQVGTFTTILYFNFCNSCVGMNRRPILIIITLMDRDGOVLGRSFEGRICACPR 300
301 DRKADEHYREQQALNESSAKNGAASKRAFQSPAPVAPALGAGVKKRRHGEDTYTLOVR 360
301 DRKADEHYREQQALNESSAKNGAASKRAFQSPAPVAPALGAGVKKRRHGEDTYTLOVR 360
361 GRENFELMKLESLELMELVPOPLVDSYRQOQLLQRPVPSYGPVLSPMNVHGG 420
361 GRENFELMKLESLELMELVPOPLVDSYRQOQLLQRPVPSYGPVLSPMNVHGG 420
421 MNKLPSVNLVQVPPPHSSAATPNLGPVGMNHNHGAHPANGEMSSSSHAQSMVSGSH 480
421 MNKLPSVNLVQVPPPHSSAATPNLGPVGMNHNHGAHPANGEMSSSSHAQSMVSGSH 480
481 CTTPPPYHADPSLSVFTGLGCPNCEIYFTSQGLSIYHLQNTIEDLGALKIPEQYRMT 540
481 CTTPPPYHADPSLSVFTGLGCPNCEIYFTSQGLSIYHLQNTIEDLGALKIPEQYRMT 540
541 IWRGLQDLKQGHYDSTAQQLRSSNAATISIGSGELQQRVMEAVHFRVHTTIPNR 600
541 IWRGLQDLKQGHYDSTAQQLRSSNAATISIGSGELQQRVMEAVHFRVHTTIPNR 600
601 GPGGGPDWADFGDLPDCKARKQPIKEEFTAEI 636
601 GPGGGPDWADFGDLPDCKARKQPIKEEFTAEI 636

RESULT 2
9XSK8

ID O9XSK8 PRELIMINARY; PRT; 637 AA.
AC O9XSK8;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE P53-LIKE TRANSCRIPTION FACTOR.
GN P73
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
OC Chlorocebus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RA CAPUT D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
FR EMBL; F11419; CAA72224.1; - S -> -
DT VARIANT 495
SQ SEQUENCE 637 AA; 69630 MW; 8F092B51 CRC32;

Query Match 97.78; Score 3304.5; DB 6; Length 637;

Best Local Similarity 97.58; Pred. No. 1e-256;
Matches 621; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVVGTTDSSMDVFHLEGMTTS 60
Db 1 MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVVGTTDSSMDVFHLEGMTTS 60
QY 61 VMAQFNLLSSTMDQSSRAASAPYTPHAAASVPTSHPSYAPQSSFTDMSAPVIPSNTD 120
Db 61 VMAQFNLLSSTMDQSSRAASAPYTPHAAASVPTSHPSYAPQSSFTDMSAPVIPSNTD 120
QY 121 YPGPHFEVTFQSSSTAKSATWYSPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180
Db 121 YPGPHFEVTFQSSSTAKSATWYSPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180
QY 181 YKKAETHVDVVKRCPNHELGRDNFEGOSAPASHLIRVEGNLSQYVDDPVTGROSVVVY 240
Db 181 YKKAETHVDVVKRCPNHELGRDNFEGOSAPASHLIRVEGNLSQYVDDPVTGROSVVVY 240
QY 241 EPPQVGTFTTILYFNFCNSCVGMNRRPILIIITLMDRDGOVLGRSFEGRICACPR 300
Db 241 EPPQVGTFTTILYFNFCNSCVGMNRRPILIIITLMDRDGOVLGRSFEGRICACPR 300
QY 301 DRKADEHYREQQALNESSAKNGAASKRAFQSPAPVAPALGAGVKKRRHGEDTYTLOVR 360
Db 301 DRKADEHYREQQALNESSAKNGAASKRAFQSPAPVAPALGAGVKKRRHGEDTYTLOVR 360
QY 361 GRENFELMKLESLELMELVPOPLVDSYRQOQLLQRPVPSYGPVLSPMNVHGG 420
Db 361 GRENFELMKLESLELMELVPOPLVDSYRQOQLLQRPVPSYGPVLSPMNVHGG 420
QY 421 MNKLPSVNLVQVPPPHSSAATPNLGPVGMNHNHGAHPANGEMSSSSHAQSMVSGSH 480
Db 421 MNKLPSVNLVQVPPPHSSAATPNLGPVGMNHNHGAHPANGEMSSSSHAQSMVSGSH 480
QY 481 CTTPPPYHADPSLSVFTGLGCPNCEIYFTSQGLSIYHLQNTIEDLGALKIPEQYRMT 540
Db 481 CTTPPPYHADPSLSVFTGLGCPNCEIYFTSQGLSIYHLQNTIEDLGALKIPEQYRMT 540
QY 541 IWRGLQDLKQGHYDSTAQQLRSSNAATISIGSGELQQRVMEAVHFRVHTTIPNR 599
Db 541 IWRGLQDLKQGHYDSTAQQLRSSNAATISIGSGELQQRVMEAVHFRVHTTIPNR 599
QY 600 GPGGGPDWADFGDLPDCKARKQPIKEEFTAEI 636
Db 600 GPGGGPDWADFGDLPDCKARKQPIKEEFTAEI 637

RESULT 3
O15351
ID O15351 PRELIMINARY; PRT; 499 AA.

AC 015351;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE P73 PROTEIN.
 GN P73.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97433090.
 RA KAGHAD M., BONNET H., YANG A., CREANCIER L., BISCAN J.C., VALENT A.,
 RA MINTY A., CHALON P., LELIAS J.M., DUMONT X., FERRARA P., MCKEON F.,
 RA CAPUT D.;
 RT "Monoclonally expressed gene related to p53 at 1p36, a region
 frequently deleted in neuroblastoma and other human cancers."
 RL Cell 90:809-814(1991)
 DR EMBL; 111416; CAA72219.17.
 DR HSP; P04637; ITRK.
 DR PFM; P00870; P53; 1.
 DR PRINTS; P00386; P53SUPPRESSR.
 SQ SEQUENCE 499 AA; 54322 MW; EB327EF3 CRC32;

Query Match 77.5%; Score 2624; DB 4; Length 499;
 Best Local Similarity 100.0%; Pred. No. 2.5e-202;
 Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQSTATSPDGGTTEHLSLEPDSYFDLPQSSRGNNVVGTDSSMDVHLEGMTTS 60
 DB 1 MAQSTATSPDGGTTEHLSLEPDSYFDLPQSSRGNNVVGTDSSMDVHLEGMTTS 60
 QY 61 VMAQNLSSTMDQMSRAASASPYTPHAAASVTHSPYAPQPSSTFTMSPAPVPSNTD 120
 DB 61 VMAQNLSSTMDQMSRAASASPYTPHAAASVTHSPYAPQPSSTFTMSPAPVPSNTD 120
 QY 121 YGPHHFEVTFQSSSTAKSATWYSPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180
 DB 121 YGPHHFEVTFQSSSTAKSATWYSPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV 180
 QY 181 YKKAHVTDVVKRCNHELGRDFNEGQSPASHLIRVEGNLSQYVDDPYTGQSVVVPY 240
 DB 181 YKKAHVTDVVKRCNHELGRDFNEGQSPASHLIRVEGNLSQYVDDPYTGQSVVVPY 240
 QY 241 EPPQVGTFTILYFNFCNSCVGGMNRRPILIIITLEMRDQVGLRRSFGRICACPR 300
 DB 241 EPPQVGTFTILYFNFCNSCVGGMNRRPILIIITLEMRDQVGLRRSFGRICACPR 300
 QY 301 DRKAMEDHYREQOALNESSAKNGAASKRAFKQSPAPVAPALGAGVKRRHGDYTYLOVR 360
 DB 301 DRKAMEDHYREQOALNESSAKNGAASKRAFKQSPAPVAPALGAGVKRRHGDYTYLOVR 360
 QY 361 GRENFELMKLESLELMELVPLVDSYRQOQQLLRQPSHLQPPSYGPLYSPMNVHGG 420
 DB 361 GRENFELMKLESLELMELVPLVDSYRQOQQLLRQPSHLQPPSYGPLYSPMNVHGG 420
 QY 421 MNKLPVNLQVGPVPPHSSAATPNLPGVPGMLNHHGAVPANGEMSSSHASQSVSGH 480
 DB 421 MNKLPVNLQVGPVPPHSSAATPNLPGVPGMLNHHGAVPANGEMSSSHASQSVSGH 480
 QY 481 CTPPPPHADPSLV 494
 DB 481 CTPPPPHADPSLV 494

RESULT 4
 ID Q9W664 PRELIMINARY; PRT; 641 AA.
 AC Q9W664;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)

DE P73
 OS Barbus barbus (barbel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprininae; Cyprininae; Barbus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BHASKARAN A., MAY D., RAND-WEAVER M., TYLER C.R.;
 RT "Fish p73, ancestral p53";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF043641; AAD27752.1;
 SQ SEQUENCE 641 AA; 71090 MW; D66F552E CRC32;

Query Match 71.4%; Score 2414.5; DB 13; Length 641;
 Best Local Similarity 70.7%; Pred. No. 2.1e-185;
 Matches 456; Conservative 81; Mismatches 91; Indels 17; Gaps 8;
 QY 4 STATSPDGGTTEHLSLEPDSYFDLPQSSRGNNVVGTT-----DSSMDVH--L 54
 DB 4 STATSPDGGTTEHLSLEPDSYFDLPQSSRGNNVVGTT-----DSSMDVH--L 54
 QY 2 SOSSTADGTTTEHLSLEPDSYFDLPQSSRGNNVVGTT-----DSSMDVH--L 61
 DB 2 SOSSTADGTTTEHLSLEPDSYFDLPQSSRGNNVVGTT-----DSSMDVH--L 61
 QY 55 EGMTTSVMAQNLSSTMDQ--MSRAASASPYTPHAAASVTHSPYAPQPSSTFTDMSAP 113
 DB 55 EGMTTSVMAQNLSSTMDQ--MSRAASASPYTPHAAASVTHSPYAPQPSSTFTDMSAP 113
 QY 62 RMDNDVNSQYSLSSSMEQGLNRAASTSPYSSTTSNVTSPYSOPNSFEAMSPAP 121
 DB 62 RMDNDVNSQYSLSSSMEQGLNRAASTSPYSSTTSNVTSPYSOPNSFEAMSPAP 121
 QY 114 VIPNTDYPGPHPEVTFQSSSTAKSATWYSPLKLYCQIAKTCPIQIKVSTPPPGT 173
 DB 114 VIPNTDYPGPHPEVTFQSSSTAKSATWYSPLKLYCQIAKTCPIQIKVSTPPPGT 173
 QY 122 AIPNTDYPGPHPEVTFQSSSTAKSATWYSPLKLYCQIAKTCPIQIKVSTPPPGT 181
 DB 122 AIPNTDYPGPHPEVTFQSSSTAKSATWYSPLKLYCQIAKTCPIQIKVSTPPPGT 181
 QY 174 AIRAMPVYKKAHVTDVVKRCNHELGRDFNEGQSPASHLIRVEGNLSQYVDDPYTGR 233
 DB 174 AIRAMPVYKKAHVTDVVKRCNHELGRDFNEGQSPASHLIRVEGNLSQYVDDPYTGR 233
 QY 182 VIRAMPVYKKAHVTDVVKRCNHELGRDFNEGQSPASHLIRVEGNLSQYVDDPYTGR 241
 DB 182 VIRAMPVYKKAHVTDVVKRCNHELGRDFNEGQSPASHLIRVEGNLSQYVDDPYTGR 241
 QY 234 QSVVVPVPEPQVGTFTILYFNFCNSCVGGMNRRPILIIITLEMRDQVGLRRSFGR 293
 DB 234 QSVVVPVPEPQVGTFTILYFNFCNSCVGGMNRRPILIIITLEMRDQVGLRRSFGR 293
 QY 242 QSVVVPVPEPQVGTFTILYFNFCNSCVGGMNRRPILIIITLEMRDQVGLRRSFGR 301
 DB 242 QSVVVPVPEPQVGTFTILYFNFCNSCVGGMNRRPILIIITLEMRDQVGLRRSFGR 301
 QY 294 ICACPRDRKADEDHYREQOALNESSAKNGAASKRAFKQSPAPVAPALGAGVKRRHGD 353
 DB 294 ICACPRDRKADEDHYREQOALNESSAKNGAASKRAFKQSPAPVAPALGAGVKRRHGD 353
 QY 302 ICACPRDRKADEDHYREQOALNESSAKNGAASKRAFKQSPAPVAPALGAGVKRRHGD 361
 DB 302 ICACPRDRKADEDHYREQOALNESSAKNGAASKRAFKQSPAPVAPALGAGVKRRHGD 361
 QY 354 TYIQLQVGRNFELMKLESLELMELVPLVDSYRQOQQLLRQPSHLQPPSYGPLY 412
 DB 354 TYIQLQVGRNFELMKLESLELMELVPLVDSYRQOQQLLRQPSHLQPPSYGPLY 412
 QY 362 MYIPLVGRNFELMKLESLELMELVPLVDSYRQOQQLLRQPSHLQPPSYGPLY 421
 DB 362 MYIPLVGRNFELMKLESLELMELVPLVDSYRQOQQLLRQPSHLQPPSYGPLY 421
 QY 413 PMNVHVGGMNKLPSVNLQVGPVPPHSSAATPNLPGVPGMLNHHGAVPANGEMSSSHAS 472
 DB 413 PMNVHVGGMNKLPSVNLQVGPVPPHSSAATPNLPGVPGMLNHHGAVPANGEMSSSHAS 472
 QY 422 NMNKHGSIKLPVNLQVGPVPPHSSAATPNLPGVPGMLNHHGAVPANGEMSSSHAS 479
 DB 422 NMNKHGSIKLPVNLQVGPVPPHSSAATPNLPGVPGMLNHHGAVPANGEMSSSHAS 479
 QY 473 QSVVSGHCHTTPPPPHADPSLVFLTGLGCPNCEIYFTSQGLQSIYHONTIEDLGALK 532
 DB 473 QSVVSGHCHTTPPPPHADPSLVFLTGLGCPNCEIYFTSQGLQSIYHONTIEDLGALK 532
 QY 480 QSVVSGHCHTTPPPPHADPSLVFLTGLGCPNCEIYFTSQGLQSIYHONTIEDLGALK 539
 DB 480 QSVVSGHCHTTPPPPHADPSLVFLTGLGCPNCEIYFTSQGLQSIYHONTIEDLGALK 539
 QY 533 IPEQYRTIKRGDLKQGHDIYTAQQLLR--SSNAATISIGGSGELQGRVNEAVHFRVR 591
 DB 533 IPEQYRTIKRGDLKQGHDIYTAQQLLR--SSNAATISIGGSGELQGRVNEAVHFRVR 591
 QY 540 IPEQYRTIKRGDLKQGHDIYTAQQLLR--SSNAATISIGGSGELQGRVNEAVHFRVR 597
 DB 540 IPEQYRTIKRGDLKQGHDIYTAQQLLR--SSNAATISIGGSGELQGRVNEAVHFRVR 597
 QY 592 HTTIPNRGPGGPPDEWDFGLDPCDKARKQPIKEEFTEAIEH 636
 DB 592 HTTIPNRGPGGPPDEWDFGLDPCDKARKQPIKEEFTEAIEH 636
 QY 598 HTTIPNRGAPTGA--EWADFGDMPDCRIHKHSIKEEFAESDVH 641
 DB 598 HTTIPNRGAPTGA--EWADFGDMPDCRIHKHSIKEEFAESDVH 641

RESULT 5
 ID Q9WUJO PRELIMINARY; PRT; 497 AA.
 AC Q9WUJO;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE P73 (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (1)
 SEQUENCE FROM N.A.
 STRAIN-D3 (129SV);
 MEDLINE; 99247549.
 HERRANZ M., SANTOS J., SALIDO E., FERNANDEZ-PIQUEAS J., SERRANO M.;
 "mouse p73 gene maps to the distal part of chromosome 4 and might be
 involved in the progression of gamma-radiation-induced T-cell
 lymphomas.";
 Cancer Res. 59:2068-2071(1999).
 EMBL; AF138873; AAD3213.1; -.
 NON_TER 1
 SEQUENCE 497 AA; 54717 MW; FFD43964 CRC32;

```
Query Match      70.3%; Score 2379; DB 11; Length 497;  
Best Local Similarity 90.2%; Pred. No. 1.1e-182;  
Matches 450; Conservative 19; Mismatches 22; Indels 8; Gaps
```

144 YSPLLAKLYCQIAKTCPIQIKVSTPPPGGTAIRAMPYVKKAHVTDVVKRCPNHELGRDF 203
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 YSPLLAKLYCQIAKTCPIQIKVSTPPPGGTAIRAMPYVKKAHEVDIVKRCPNHELGRDF 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
204 NEGQSAPASHLIRVEGNLSOYDDPVTGRQSVVVYPPEPVGTFTTILNFMCNSSCV 263
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 NEGQSAPASHLIRVEGNLAQYDDPVTGRQSVVVYPPEPVGTFTTILNFMCNESSV 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
264 GGMNRPIIITLEMRGOVLGGRRSEGRICACPGDRKADEHYRQQALNSSSAKN 323
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 GGMNRPIIIVITLTDRGOVLGGRRSEGRICACPGDRKADEHYRQQALNESTTKNG 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
324 AASKRAFKOSPAPVALCAGYKKRRHGDETYTLQV - RGRENFEIMLMKESLEMLVP 362
| | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | |
181 AASKRAFKOSPPAIPALCTNVKKRRHGDEMFMHYSARGENFELMKVKSLEMLVP 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
383 QPLVDSYR -- QQOQLLRPSHLQPPSYGPLVSPMNVHGVGMNKLP SVNQLVGQPPPHTSSA 440
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 QHLVDSYRQQOQLLRPSHLQPPSYGPLVSPMNKHGVGNKLPSVNQLVGQPPPHTSSA 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
441 ATPNLGPVGPGLNNHHAVPANEMSSSHASQSVSGHSCHCTTPPPPYHADPSLVSFUTGL 500
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 AGPNLPGMSGMLNSGHSMSPANGEMMGNHSSQTMYSGSHCTPPPPPYHADPSLVSFUTGL 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501 GCPCNCLEYTSOGLOSIIYHLONLIETDLGALKTIPEORYMTINWRGLDKKGCHDYSTAQOL 560
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 GCPCNCECTSOGLSIIYHLONLIETDLGALKVPDQRYMTINWRGLDJKQSHD -- CGCQL 418
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
561 LR--SSNAATISIGGSSELQRORVMVAHFVRRTIIPNRGGPGG--GPSDWADFQDLP 617
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
419 LRSSSNAATISIGGSSELQRORVMVAHFVRRTIIPNRGGAGAYTGPDWADFQDLP 478
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
618 DCKARKQPKEEFTAETH 636
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
479 DCKSRKPKEEFTEESH 497
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

SULT 5
3898 PRELIMINARY; PRT; 680 AA.
O8898;
O8898; (TREMblrel. 08, Created)
01-NOV-1998 (TREMblrel. 08, Last sequence update)
01-NOV-1998 (TREMblrel. 08, Last sequence update)
01-NOV-1999 (TREMblrel. 12, Last annotation update)
TA-p63 ALPHA.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1] SEQUENCE FROM N. A.
MEDLINE; 9844805.
YANG A., KAGHAD M., GILLET E., FLEMING M.D., DOTSCH V., ANDREWS N.C.
CAPUT D., MCKEON F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with

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transactivating, death-inducing, and dominant-negative activities." ;
RT      ML. Cell 2:305-316(1998).
RL      EMBL; AF075436; AAC62641.1; -.
DR      HSSP; P04637; 1YCS.
DR      PFAM; PF00870; P53; 1.
DR      PRINTS; PRO0386; P53SUPPRESSR.
DR      SEQUENCE 680 AA; 7678 MW; 230EDIFA CRC32;

Query Match          52.9%; Score 1789; DB 11; Length 680;
Best Local Similarity 55.1%; Pred. No. 3e-135;
Matches 366; Conservative 94; Mismatches 144; Indels 60; Gaps

QY      1 MAQSTAT----SPDGGTTFEHLKSSLEP-----DSTYFDLPQSGRGNNEVVGTTDSS 48
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      49 MDVFLEGNWTS-----VMAQFNLLSSTMDQSSRAASAPYTPPEHAA-SVPHSSPYAQ 102
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      93 MDCIRMDSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSYNTDHAQNSVTAPSPYAQ 152
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      103 SSTFTMSPAVIPSNITDPGPHHFETVTFQGSTAKSATWTYSPLLKAKLCQAKTCTPTQ 162
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      153 SSTFDALSPSAPSNITDPGPHSFDVSFQGSSTAKSATWTYSTELAKLCQAKTCTPTQ 212
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      163 IKVSTPPPPGTAIRAMPVYKKAASHYTDVVYKRCNHELGRDNFEGQSAPASHLIRVGNL 222
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      213 IKWITPPPGQAVIRAMPVYKKAASHYTVVYKRCNHELGRDNFEGQIAPPSHLIRVEGNSH 272
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      223 SOYVDDPVTGRQSVVVPYEPPOVGTFTILYNFNCSSCVGGNNRRPILIIITLEWRDG 282
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      273 AQYVEDPTGRQSVLYPEPPQVGTFTILYNFNCSSCVGGNNRRPILIIITLEWRDG 332
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      283 QVIGRRSFEGRICACPGDRKKADEHYREQQALNESSAKGAASKRAFQSPPAFALGA 342
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      333 QVIGRRSFEGRICACPGDRKKADEHSIRKQV--SDSAKNGDGTKRPFQNTHTGIQW--T 388
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      343 GVKRRHGHDETTYLYVGRGENFEILMKLESLELWLPQPLVDYSVRQOQQ-----LLQ 397
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      389 STKKRRSPDDELLYLVPRGREYEMLLKIKESLELMQYLPQHTIETVYRQOQQOHOHLQ 448
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      398 RPSHLQ-PPSYGPVLPMNKVHGNNKLPVSNQLVGPPPHSSAATPNLGFVGFG-----M 452
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      449 KOTSQOSQSYGNSPPLANKN-SMNKLPVSQLIN--PQORNALPTTTTPEGAGANIP 505
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      453 LNNHGHAVPANGEMSSSSHAQ-----SMVSGSHTCTPPVYHADPSLVSLTGLGCPNCI 506
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      506 MGTH---NPVANGDUNGSLPTQALPPLSPWSTSHCTPPPPYPTDCSIVSLARLGSCCL 562
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      507 EYFTSQLSQSYHLQNLTDLGALKIPEQYRMTIWRGLQDLKQGHDSYTAQOLLRS-SN 565
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      563 DYFTTQGLTTIQTIEHYSMDLASKIPEQFRHAIWKGLDHRQLHDFSSPHLLRTPSG 622
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      566 AATISGSGELQQRQVMEAVHFRVYRHTTITPNRGGPGGPDWADGDLDPCKARKQP 625
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      623 ASTVSV-GSSTRGERVIDAVRFTLQRTISPPPR-----DEWDFNFDMDSRNRKQQR 674
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      626 IKEE 629
Db      1 : : : :
QY      675 IKEE 678
Db      1 : : : :

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RESULT	7
ID	O75195 PRELIMINARY; PRT; 641 AA.
AC	O75195;
DT	01-NOV-1998 (TRENBLrel. 08, Created)
DT	01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT	01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE	P51B.
OC	DE Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Eutheria; Primates; Catarrhini; Hominoideae; Homo.

[1]
RN SEQUENCE FROM N.A.
RP TISSUE-SKELETAL MUSCLE;
RX MEDLINE; 98324755.
RA OSADA M., OHBA M., KAWAHARA C., ISHIKAWA R., KATOH I.,
RA IKAWA Y., NIMURA Y., NAKAGAWARA A., OGINATA M.,
RT "Cloning and functional analysis of human p51, which structurally and
RT functionally resembles p53."
RL Nat. Med. 4:839-844(1998).
DR EMBL; AB016073; BAA32593.1; -.
DR HSP; P04637; 1YCS.
DR PFAM; PFO0870; P53; 1.
DR PRINTS; P00386; P53SUPPRESSOR.
SQ SEQUENCE 641 AA; 72019 MW; 2818F74C CRC32;

Query Match 52.8%; Score 1786; DB 4; Length 641;
Best Local Similarity 55.0%; Pred. No. 4.8e-135;
Matches 365; Conservative 94; Mismatches 145; Indels 60; Gaps 18;

QY 1 MAOSTAT-SPDGGTTFEHLWSSLEP-----DSTYFDLPQSSRGNNVVGTTSS 48
DB 1 MSSTQTNELSPF-VFQHIWDFLEQICSVQPIDLNFVDEPSENGATNKI-----EIS 53
QY 49 MDVHLEGMTS-----VMAQFNLLSTMDQSSRAASAPYTPHAA-SVTPHSPYAP 102
DB 54 MDCIRMDSDLSDPMPQYTNLGLLNMDOQIQNGSSSTSPYNTDHAQNSVTAPSPYAP 113
QY 103 SSFDMSPAPVPSNTDYPGPHFEVTFQOSTAKSATWYSPLLKLYCOIATCPIQ 162
DB 114 SSFDMSPAPVPSNTDYPGPHFEVTFQOSTAKSATWYSPLLKLYCOIATCPIQ 173
QY 163 IKVSTPPPGTAIRAMPVYKAEHVDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNL 222
DB 174 IKVSTPPPGTAIRAMPVYKAEHVDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNL 233
QY 223 SQYVDDPVTGRQSVVYPPQVGTFTILYFNCNCSVCGMNRRLIITVLETRDG 282
DB 234 AQVDEPITGRQSVVYPPQVGTFTILYFNCNCSVCGMNRRLIITVLETRDG 293
QY 283 QVLRGRFEGRICACGRORKADEHYREQQALNESSAKRAKQSPVAPALGA 342
DB 294 QVLRGRFEGRICACGRORKADEHYREQQALNESSAKRAKQSPVAPALGA 349
QY 343 GVKRRHGEDTYYLVQVRENFELMKLESLELMELVQPLVDSYRQOQO-----LLQ 397
DB 350 SIKRRSPDDELLYLVQVRENFELMKLESLELMELVQPLVDSYRQOQO-----LLQ 409
QY 398 RPSHLQ-PPSYGVLSPMKNVHGNNKLPVNLQVQPPHSSAATPNLGPVGP-...M 452
DB 410 KQTSISPSYGNSSPPLNKN-SMKNLPSVQLIN--PQORALTPPTDGMGANIPM 466
QY 453 LNNHGHAVPANGEMSSSSSAQ-----SMVSGSHCTPPPPYHADPSLYFTGLGCPNCI 506
DB 467 MGTN--MPMAGDMGLSPTQALPPPLSPSTSHCTPPPPYHADPSLYFTGLGCPNCI 523
QY 507 EYTSQGLQSIYHLQNTLTDIGALKIPEQYRMTWRGLQDLKQCHDYSTAQQLRS-SN 565
DB 524 DYFTTGLTIIQIHYSDMLASLKIPEQYRMTWRGLQDLKQCHDYSTAQQLRS-SN 583
QY 566 AATISIGSGELQQRVMEAVHFRVHTTIPNRRGPGGPDDEADFGDLPDCKARKQKEE 625
DB 584 ASIVSV-GSSEIRGERVIDAVRFTLRQTSIFPPR-----DEWDFNDFMDARRNKOOR 635
QY 626 IKKE 629
DB 636 IKKE 639

RESULT 8
O35834
ID O35834 PRELIMINARY; PRT; 634 AA.
AC O35834;

DT 01-JAN-1998 (TREMREL. 05, Created)
DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
DE 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE KET PROTEIN (FRAGMENT).
GN KET.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-LINGUAL EPITHELIUM;
RX MEDLINE; 97460723.
RA SCHWALE H., BAMBERGER C.;
RT "A novel protein with strong homology to the tumor suppressor p53."
RL Oncogene 15:1363-1367(1997).
DR EMBL; Y10258; CAA71308.1; -.
DR HSP; P04637; 1YCS.
DR PFAM; PFO0870; P53; 1.
DR NON_TER 1
SQ SEQUENCE 634 AA; 71360 MW; D45E080D CRC32;

Query Match 52.5%; Score 1777; DB 11; Length 634;
Best Local Similarity 55.3%; Pred. No. 2.5e-134;
Matches 361; Conservative 92; Mismatches 144; Indels 56; Gaps 17;

QY 8 SPDGGTTFEHLWSSLEP-----DSTYFDLPQSSRGNNVVGTTSSMDVHLEGMTT 59
DB 5 SPF-VFQHIWDFLEQICSVQPIDLNFVDEPSENGATNKI-----EISMDCTRMQSD 57
QY 60 S-----VMAQFNLLSTMDQSSRAASAPYTPHAA-SVTPHSPYAPSTFTDWSAP 113
DB 58 SDPMWPQYTNLGLLNMDOQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSTFDALSP 117
QY 114 VPSNTDYPGPHFEVTFQOSTAKSATWYSPLLKLYCOIATCPIQIKVSTPPPGT 173
DB 118 AIPSNTDYPGPHFEVTFQOSTAKSATWYSPLLKLYCOIATCPIQIKVSTPPPGT 177
QY 174 AIRAMPVYKAEHVDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLQYVDDPVTGR 233
DB 178 VIRAMPVYKAEHVDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLQYVDDPVTGR 237
QY 234 QSVVYPPQVGTFTILYFNCNCSVCGMNRRLIITVLETRDGQVLRGRFEGR 293
DB 238 QSVVYPPQVGTFTILYFNCNCSVCGMNRRLIITVLETRDGQVLRGRFEGR 297
QY 294 ICACGRORKADEHYREQQALNESSAKRAKQSPVAPALGAGVKKRRRGGED 353
DB 298 ICACGRORKADEHYREQQALNESSAKRAKQSPVAPALGAGVKKRRRGGED 353
QY 354 TYLVQVRENFELMKLESLELMELVQPLVDSYRQOQO-----LLQPSHLQ-PPSY 407
DB 354 LLYLVQVRENFELMKLESLELMELVQPLVDSYRQOQO-----LLQPSHLQ-PPSY 413
QY 408 GPVLSPMKNVHGNNKLPVNLQVQPPHSSAATPNLGPVGP-...MLNNGHAPVAN 463
DB 414 GNSPPLNKN-SMKNLPSVQLIN--PQORALTPPTDGMGANIPMGTN--MPMA 467
QY 464 GNSPPLNKN-SMKNLPSVQLIN--PQORALTPPTDGMGANIPMGTN--MPMA 517
DB 468 GDMGLSPTQALPPPLSPSTSHCTPPPPYHADPSLYFTGLGCPNCI 527
QY 518 YHLQNTLTDIGALKIPEQYRMTWRGLQDLKQCHDYSTAQQLRS-SNATISIGSGE 576
DB 528 YQIHYSDMLASLKIPEQYRMTWRGLQDLKQCHDYSTAQQLRS-SNATISIGSGE 586
QY 577 LQORVMEAVHFRVHTTIPNRRGPGGPDDEADFGDLPDCKARKQKEE 629
DB 587 TRGERVIDAVRFTLRQTSIFPPR-----DEWDFNDFMDARRNKOOR 632

RESULT 9
O89097

089097; PRELIMINARY; PRT; 586 AA.
089097;
01-NOV-1998 (TREMELrel. 08, Created)
01-NOV-1998 (TREMELrel. 08, Last sequence update)
01-NOV-1999 (TREMELrel. 12, Last annotation update)
DN P63 ALPHA.
P73H.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
MEDLINE: 98448095.
YANG A., KAGHAD M., GILLET E., FLEMING M.D., DOTSCH V., ANDREWS N.C.,
CAPUT D., MCKEON F.,
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities,"
Mol. Cell 2:305-316(1998).
[2]
SEQUENCE FROM N.A.
TISSUE=THYMUS;
MEDLINE: 98389596.
SENCO M., SEKI N., OHIRA M., SUGANO S., WATANABE M., TACHIBANA M.,
TANAKA T., SHINKAI Y., KATO H.,
"A second p53-related protein, p73L, with high homology to p73,"
Biochem. Biophys. Res. Commun. 248:603-607(1998).
EMBL: AF075439; AAC62644.1; -
EMBL: AB010152; BAA32432.1; -
HSSP: P04637; 1YCS.
PFAM: PF00870; P53; 1.
PRINTS; PRO0386; P53SUPPRESSOR.
SEQUENCE 586 AA; 65789 MW; 2C644135 CRC32;
Query Match 51.5%; Score 1743; DB 11; Length 586;
Best Local Similarity 59.7%; Pred. No. 1.2e-131;
Matches 347; Conservative 82; Mismatches 116; Indels 36; Gaps 13;
QY 67 LLSSTMDQSSRAASASPTPEHAA-SVPTHSYAPQSTFTDMSAPVIPSNTDYPGPH 125
DB 22 LLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSTFDALSPSPAIPSTNDYPGPH 81
QY 126 HFEVTFQOSTAKSATWYSPLLKLYCQIAKTCPTQIKVSTPPPGTAIRAMPYKAAE 185
DB 82 SDFVSFQOSTAKSATWYSTELKKLYCQIAKTCPTQIKVSTPPPGTAIRAMPYKAAE 141
QY 186 HVTDVYKRCPNHGLRDNFNEGQAPASHLIRVEGNLSQYDDPVTGROSVVYVPEPQV 245
DB 142 HVTDVYKRCPNHGLRDNFNEGQAPASHLIRVEGNLSQYDDPVTGROSVVYVPEPQV 201
QY 246 GTEFTTILYFNCNCSVCGMNRRLIITLLEMRGOVLGRSRFEGRICACPGDRKAD 305
DB 202 GTEFTTILYFNCNCSVCGMNRRLIITLLEMRGOVLGRSRFEGRICACPGDRKAD 261
QY 306 EDHYREQQALNESAAGAKRAFPKQSPAPVAPALGAGVKRRHGDDEDTYLVQVGRGNF 365
DB 262 EDSIRKQV--SDSAKNGDGTKRFRQNTGHIQM--TSIKRRSPDDELLYLVGRGRTY 317
QY 366 EILMKLESLELMELVPOPLVDSYRQOQ-----LLQRPESHQ--PPSYGVLPSPMKVHG 419
DB 318 EMLLKIKESLELMOYLPOHTIETRYRQOQOQHLLQKQTSIQSSYSGNSPPLNKN- 377
QY 420 GNMKLPSVNLGVGPPHSSAATPNLGPVGP-----MLNHHGAVPANGEMSSSSHAQ-- 474
DB 377 SNMKLPSVQLIN--PQORNALPTTTPMGANGINIPMGTH--MPMAGDMGLSPTQAL 431
QY 474 ----SNVSGSHCTPPPPYHADPSLVSLFTGLGCPNCIEYFTSQGLSIYHLQNLTIDLG 529
DB 432 PPPLSMPTSHCTPPPPYPTDCSVFSLARLGCSCLDYFTTQGLTTIYIHYSMDDLA 491
QY 530 ALKIPQRYMTWIRGLQDLKQGHYDSTAQQLRS--SNAATISIGSGELQORVMEAVHF 588
DB 492 SLKIPQRYMTWIRGLQDLKQGHYDSTAQQLRS--SNAATISIGSGELQORVMEAVHF 550
QY 589 RYRHTTIPNRRGGCGGDEWADFDFDLPDCKARKQPIKEE 639

Db 551 TLRQTISFP--DEWDFNFDMDARRNKQRIKEE 584

RESULT 11

076078
076078 ID 076078 PRELIMINARY; PRT; 448 AA.
AC 076078
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TA P63 GAMMA.

Query Match 38.3%; Score 1297.5; DB 4; Length 448;
Best Local Similarity 61.4%; Pred. No. 4.1e-96;
Matches 258; Conservative 47; Mismatches 84; Indels 11; Gaps 9.

RESUIT 12

Q88897	PRELIMINARY;	PRT;	483 AA.
ID	O88897		
AC	O88897;		
DT	01-NOV-1998 (TREMblrel. 08, Created)		
DT	01-NOV-1998 (TREMblrel. 08, Last sequence update)		
DT	01-NOV-1999 (TREMblrel. 12, Last annotation update)		
DE	TA*P63 GAMMA.		
DE	Mus musculus (Mouse).		
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 98448095.		
RA	YANG A., KASHAD M., GILLET E., FLEMING M.D., DOTSCH V., ANDREWS N.C.,		
RT	CAPUT D., MCKEON F.;		
RT	"p63, a p53 homolog at 3q27-29, encodes multiple products with		
RT	transactivating, death-inducing, and dominant-negative activities."		
WL	Mol. Cell 2:305-316(1998).		
DR	EMBL; AF075434; AAC62639.1;		
DR	HSSP; P04637; IYCS.		
DR	PFAM; PF00870; P53; 1.		
DR	PRINTS; PRO0386; P53SUPPRESSR.		
DR	SEQUENCE 483 AA; 54969 MW; 4AF2A2C4 CRC32;		

Query Match 38.0%; Score 1284.5; DB 11; Length 483;
Best Local Similarity 56.7%; Pred. No. 5e-95;
Matches 267; Conservative 50; Mismatches 91; Indels 63; Gaps 13;

RESULT 13

	PRELIMINARY;	PRT; 393 AA.
O75922	ID O75922	
AC	O75922;	
DT	01-NOV-1998 (TReMBLrel. 08, Created)	
DDT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)	
DDT	01-NOV-1999 (TReMBLrel. 12, Last annotation update)	
DE	DN P63 GAMMA.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.	

DB	101	DMPVSSPYSPHDHVSQPPSPSNIKYPGEYVFEMSFQSKETKSTTWTYSEKLDKLY	160
QY	153	CQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHEVTDVVKRCPNHELGRDFNEGQSAPAS	212

